OME Taxonomy

Our Algorithm

The goal of this lesson is to show you the OME organization of bacteria. The traditional method of organizing bacteria is based on the laboratory diagnostic algorithm. This is a very valid way to do it. More complex taxonomies have been developed based on molecular testing, genetics, and the like. All great for microbiologists. You are not a microbiologist. We need microbiologists to hold onto the microbiology, to call on them for taxonomy changes, to be the specialists in that field. We also need doctors. We need doctors to make the right clinical decision and understand why those decisions are being made. So what we do is simplify the categorization and focus more on disease than on microbiology. You still have to know which organism is Gram-positive this, Gram-negative that, which have capsules, which are (an)aerobic, which are (im)motile, and which tests separate specific species. But learning those details only when it's necessary, as part of the disease's illness script, helps alleviate the burden of information. We categorize things to facilitate recall, to make them easier to learn, and easier to retrieve later. We cover two common methods—dare we say, pitfalls—that students use to attempt microbiology, showing the folly of their structure and providing a better alternative: the OME taxonomy of bacteria.

We do this because many of you will have learned microbiology the way everyone else teaches it. The problem with that is that the people who continue to teach it the wrong way have mastered it, so it is the right way to them. They forget what it was like to study it for the first time. In education, that's called tacit—they know it so well they forget how to teach you to get to where they are. We don't want you mastering the way the masters do it; you will never be a microbiology master (they have PhDs in microbiology). You need to master the way that makes sense for you to learn it, so you become a master of clinical microbiology, not of laboratory microbiology.

Wrong Way #1: Memorizing a Table

This is how many students learn bacteria. They recite the bug name and all of its features. Each bacterium is a new line item, every feature unique to the bug, carefully sculpted details attached to that bug and that bug only. This is thorough, but induces a heavy burden of information.

Staph. aureus is Gram-positive cocci that grow in clusters. It is catalase positive and coagulase positive. The cocci have a capsule. They are immotile and aerobic. *Staph. aureus* can be sensitive to methicillin (MSSA) or resistant (MRSA). It causes skin infections, bone infections, abscess, and endocarditis.

Staph. epidermitis is Gram-positive cocci that grow in clusters. It is catalase positive but coagulase negative. The cocci do not have a capsule. They are immotile and aerobic. *Staph. epidermitis* does not grow in the presence of novobiocin. It causes central venous catheter infections.

Staph. saprophyticus is Gram-positive cocci that grow in clusters. It is catalase positive but coagulase negative. The cocci do not have a capsule. They are immotile and aerobic. *Staph. saprophyticus* does grow in the presence of novobiocin. It is a skin contaminant.

Strep. pyogenes is Gram-positive cocci that grow in chains. It is catalase negative and coagulase negative. The cocci have a capsule. They are immotile and aerobic. *Strep. pyogenes* does not grow in the presence of bacitracin. It is known as group A strep. It causes impetigo, cellulitis, and pharyngitis.

Strep . . . ZOMFG STOP.

OME's Fix for Wrong Way #1

Listen (or, I guess, read) how different this next version is from the one above.

All Gram-positive cocci are either strep or staph. All staphs grow in clusters and are catalase positive. Only *Staph. aureus* is coagulase positive. It can be MSSA, MRSA, or VRSA. Of the other staph species, the coag-negative staphs, which are usually contaminants, the only one that really matters is *epidermidis* because it can cause catheter-related infections. On laboratory diagnosis, it dies in the presence of novobiocin because *epidermidis* is sensitive to novobiocin.

All streps grow in chains and are catalase negative. You need to be able to split streps into three categories: β-hemolytic streps (complete hemolysis, *pyogenes* and *agalactiae*, separated by bacitracin), α-hemolytic streps (partial hemolysis, *Strep. pneumo* and viridans, separated by optochin), and γ-hemolytic streps (no hemolysis, *enterococcus*).

By **clustering**, the OME presentation frees up an immense amount of brain space, limiting the amount of memorization on the microbiology, allowing you then to focus on the diseases the bacteria cause.

Wrong Way #2: Following the Wrong Algorithm

Microbiologists and very good review resources for board examination preparation have made some pretty good diagnostic algorithms. Some even have fill-in-the-blank so you can make sure you can fill them in exactly as they have them drawn. That is exceptional, if your goal is to determine the genus and species in the lab, as microbiologists do. As the people working in the micro lab at the hospital do. As they do *for you*. You ARE expected to know the details about shape and color, and which sugars are fermented by which bug. But learning the algorithm as the primary way of memorizing the contents of microbiology prepares you for the role that other people do for you, and this is why it is so confusing. Try out Figure 5.1, for example.

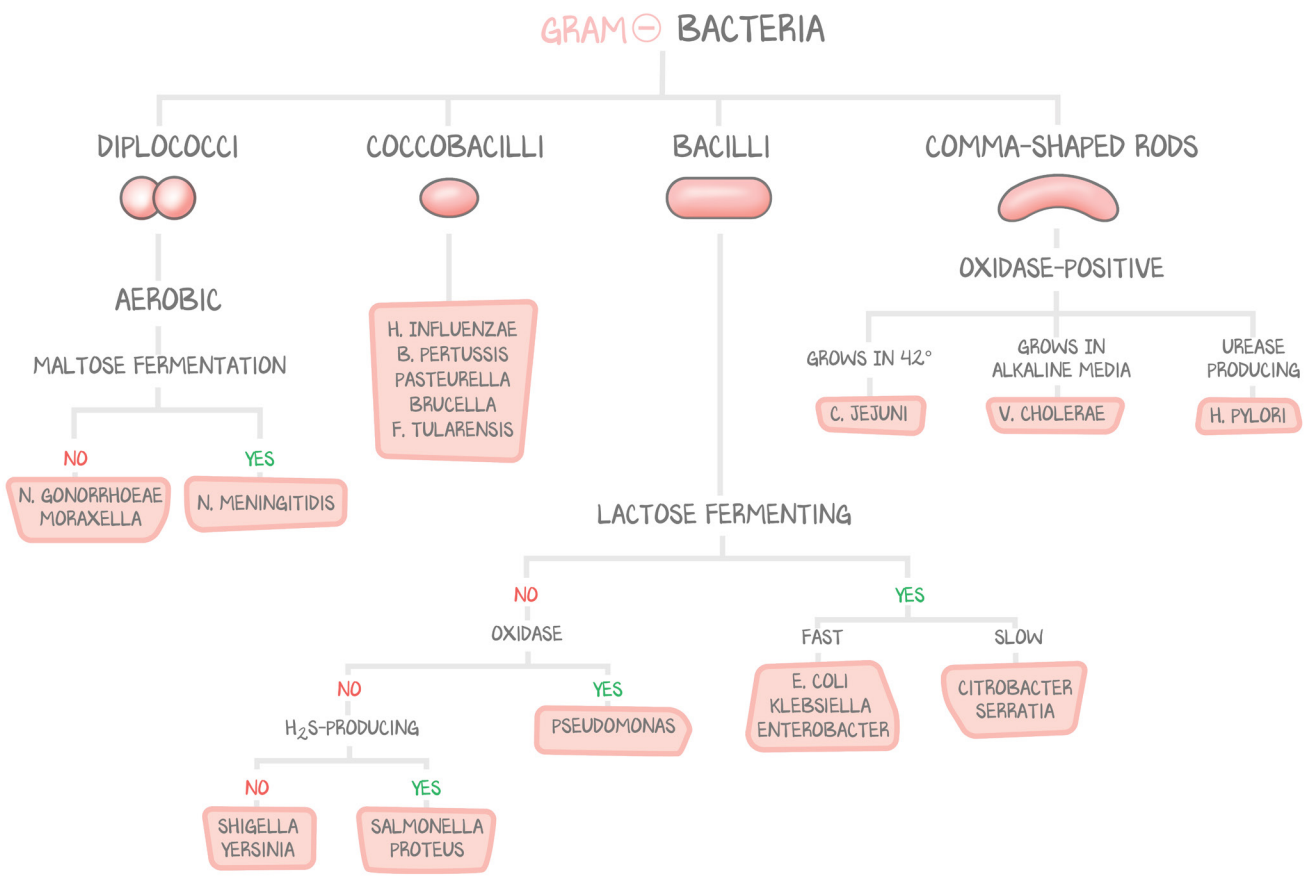

Figure 5.1: The Traditional Laboratory Diagnostic Algorithm
This is how the content has traditionally been organized. And it illustrates our point perfectly. On this diagram, which bugs cause diarrhea? *Shigella*, *Yersinia enterocolitica*, *Salmonella*, *E. coli*, *Vibrio cholerae*, and *Campylobacter*. That's right, spanning almost every branch point from the bottom left to the top right (excluding *Pseudomonas*). This is an appropriate way to organize things. It just isn't the best way for a student of medicine.

Pretty. Organized. Looks helpful, right? But what does H_2S production on TSI agar get you? *Salmonella* vs. *Shigella*. Right. Both cause dysentery. *Yersinia* vs. *Proteus*. Uh . . . *Yersinia enterocolitica* (causes diarrhea) or *Yersinia pestis* (causes plague, transmitted by animals)? BOTH! Yes . . . neither *Yersinia enterocolitica* or *Yersinia pestis* show H_2S on TSI agar. But how is that useful to you, learning disease, when one is in the context of poop bugs that cause poop disease while another is in the context of causing the bubonic plague!? When you see a bubo and start an aminoglycoside, is it the TSI agar you will be looking out for? And if the TSI agar has no H_2S (that is a negative finding that is true of all other bacteria), does it help you start the aminoglycoside?

Or how about this. Remember that table you built (or read) that compares *Salmonella* to *Shigella*? Why did you build that table? Why is it "*Salmonella* and *Shigella*?" Because they are both Gram-negative rods, do not ferment lactose, invade through M cells in Peyer patches, and can be separated from one another by the presence of black pigment on TSI agar (*Salmonella* makes H_2S; *Shigella* doesn't). Take a gander there at the table again. What ELSE is similar? Nothing. Absolutely nothing. Learning them as *Salmonella* and *Shigella* and comparing them in the same table serves only to confuse the two, your brain easily mixing up the elements on the table. One is transmitted in poultry, causes a watery diarrhea, requires a high infectious dose, and can colonize the gallbladder. The other is transmitted fecal-oral, causes a bloody diarrhea, requires a low infectious dose, and can cause HUS. There is no overlap of the two organisms except in their microbiology. We do not compare Salmonella and Shigella because their clinical picture is so vastly different.

OME's Fix for Wrong Way #2: Gram-Negative Taxonomy

You will never sit in front of a patient with a urinary tract infection and think, "I think I should look at the aerobic bottle and see if this organism is oxidase positive." You WILL get a preliminary culture back, without organisms and sensitivities yet identified, that reports Gram negative, lactose fermenters. You will then start antibiotics that cover *E. coli* and *Klebsiella* based on that information. But you will also be asked on exams to know the laboratory microbiology. But memorizing the laboratory algorithm does nothing to help you comprehend the disease they cause. If you memorize the algorithm, you are left with that being your foundation. And when asked to quickly pull an antibiotic of choice, you have to mentally trace your way down the algorithm, find your bug, and access the details. Instead, we ask you to start with the disease, organize the bugs by the problems they cause. This way you remove the step of tracing down the diagnostic algorithm and jump right to the organism, the disease presentation, and the treatment. You will have to fish around for the microbiology details as you would have to fish for the diseases' details if you memorized the microbiology first. But guess what you are going to do for the rest of your career? Diagnoses, disease presentations, and antibiotic selection, and NOT microbiology laboratory diagnostics. Learn it the right way first, with a clinical perspective.

For Gram negatives, we start off by separating everything into **definitely cocci** and everything else, aka **rods** (see Figure 5.1 again for why). Lesson #7: *Gram-Negative Cocci* covers all the medically relevant . . . you guessed it . . . Gram-negative cocci. Because they are contained in that lesson, you know they are all Gram-negative cocci, freeing you to learn the diseases they cause. Then, instead of using any biologic or laboratory feature, we categorize organisms by their special circumstances. Lesson #9: *GNR That Cause Diarrhea* is about the bacteria that cause diarrhea and express enterotoxins. Lesson #10: *GNR Transmitted by Animals* covers the low-yield but obviously animal-associated bacteria. Lesson #11: *GNR: Spirochetes* covers the diseases caused by spirochetes: syphilis, Lyme, and leptospirosis. Lesson #12: *GNR: Intracellular Obligate Parasites* covers the organisms that share common infection and treatments because they are inside host cells, with an emphasis on *Chlamydia* and *Rickettsia* species. Then everyone else, all the Gram-negative rods that weren't accounted for, the ones that cause the bad UTIs and abdominal infections, are covered in Lesson #8: *GNR That Cause Serious Disease* where the major distinction is between aerobes (*Pseudomonas*) and facultative anaerobes (*Proteus*, *E. coli*, and *Klebsiella*). This is the "bugs left over" category, and you may be wondering why it's lesson #8 and not lesson #14. It is because these are the bacteria that cause acute infections that you will deal with on a regular basis in clinicals. Pneumonia, urinary tract infections, diverticular abscesses—these are the infections of your clinical years, and so they are taught up front and first.

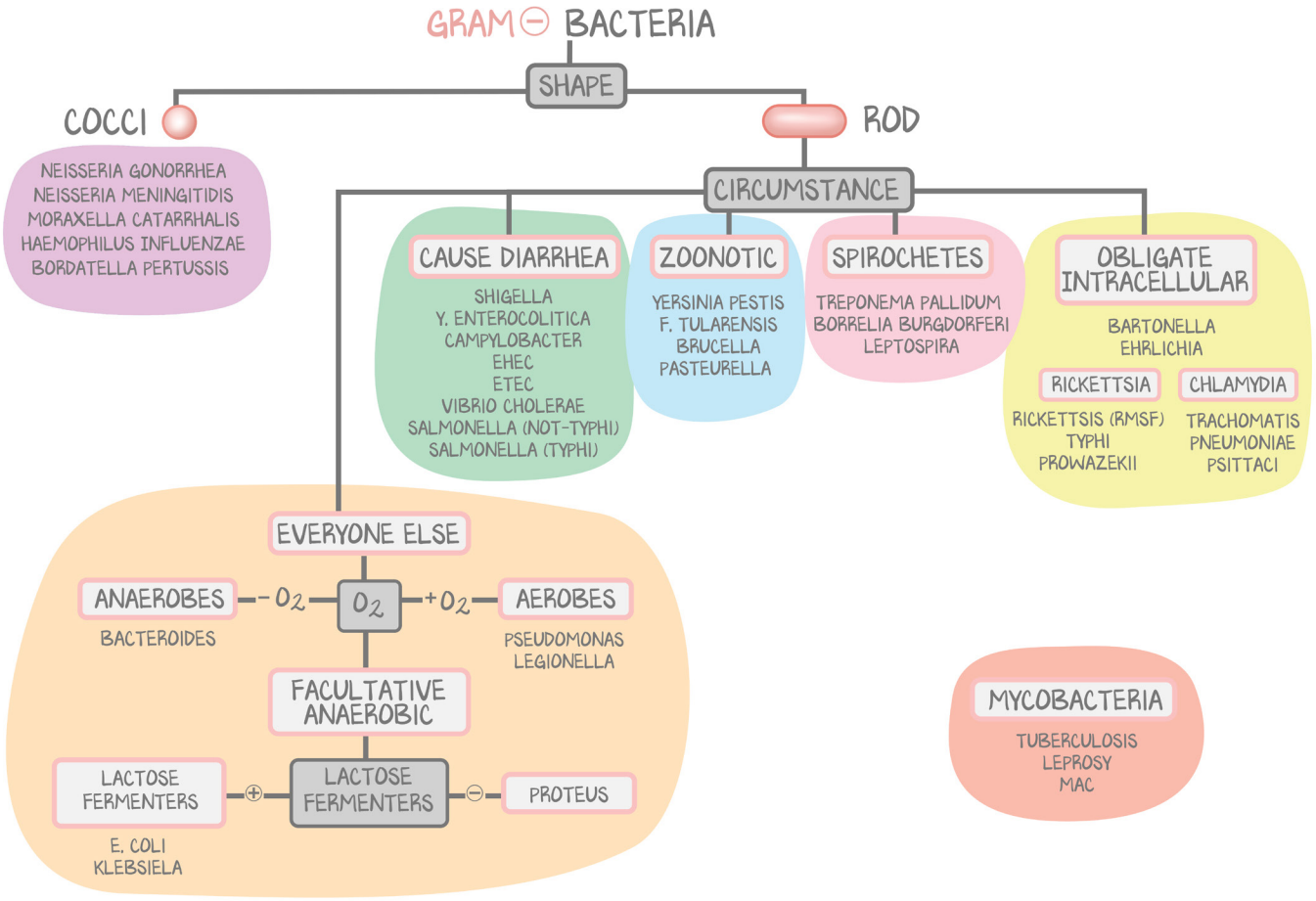

Figure 5.2: OME Gram-Negative Organization
Visualizing our simplified version which takes the micro lab out of the organization equation.

OME's Gram-Positive Organization

For strep and staph, read the first page *OME's Fix for Wrong Way #1* then look at Figure 5.3. You see how we organized the algorithm into (S) on the bottom, sensitive to the antibiotic that separates two species, and the resistant organism on top.

For Gram-positive rods, there are either spores (*Clostridium* and *Bacillus*) or not-spores. The spore species are separated by their toxins, motility, and anaerobic or not. The not-spores either branch (*Nocardia* and *Actinomyces*, commonly tested against each other) or don't branch (*Listeria* and diphtheria). But notice how we didn't use H_2S, or even try to use the same green bubble as a decision point for the different branches. The reason we didn't do that is because it doesn't make sense to do it that way. The decision tree is specifically whatever is relevant to that cluster of organisms—(an)aerobic growth for spore formers, branching for non-spore formers.

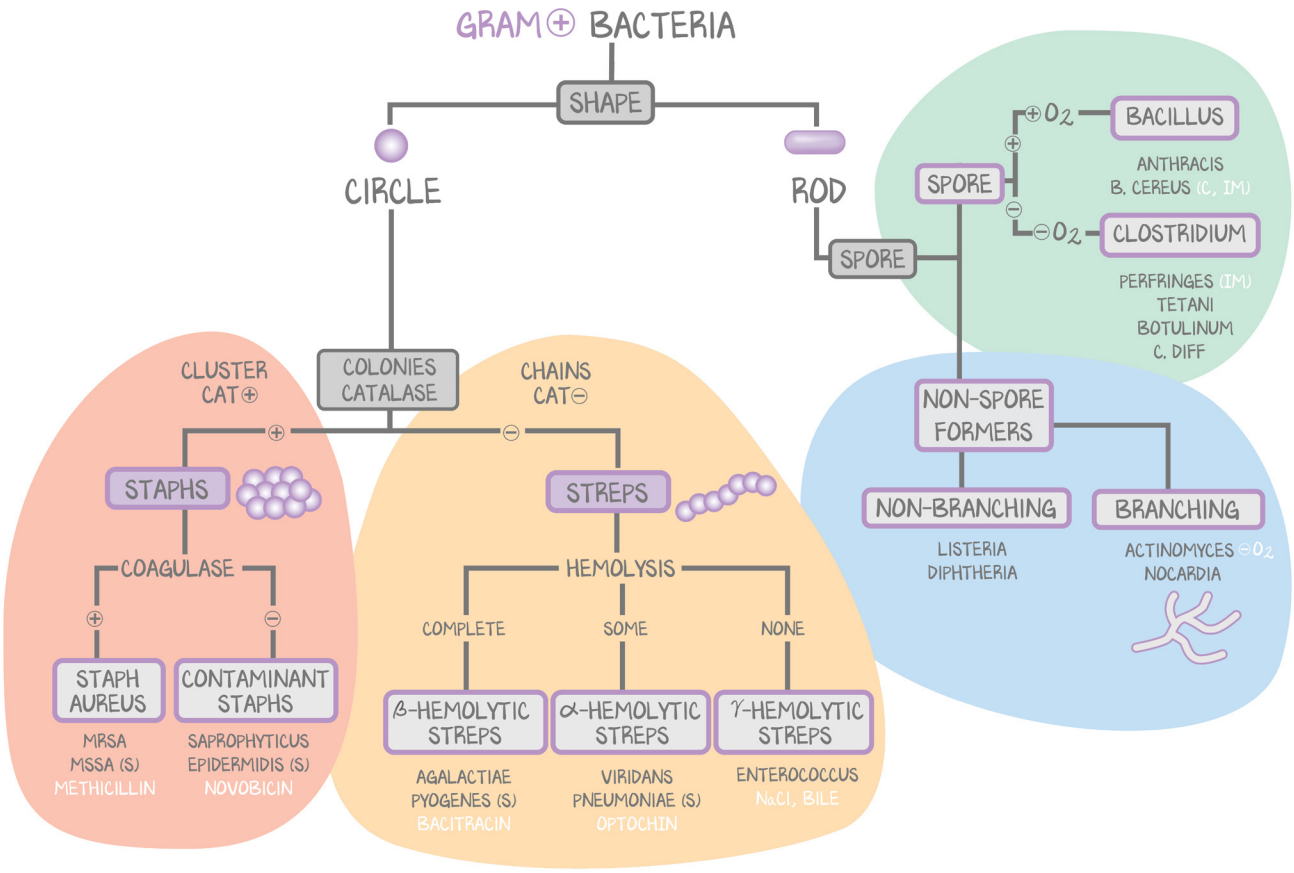

Figure 5.3: OME Gram-Positive Organization
Visualizing our simplified version which takes the micro lab out of the organization equation . . . except where it's needed, called out in white.

Putting the OME Taxonomy Together

Watch how the organizer dips in and out from species to genus, from name to disease. This is how we learned it. Instead of a bunch of Latin that didn't make sense, here's how our brains organized the material.

1. Gram-positive cocci are *Strep*. and *Staph*.
2. Gram-negative cocci are *Neisseria* species and the other *Strep. pneumo* bugs (*Haemophilus* and *Moraxella*).
3. Gram-positive rods are either spore-formers (*Clostridium* and *Bacillus*) or not (*Listeria*, diphtheria, *Nocardia*, and *Actinomyces*).
4. Gram negatives that cause serious disease are in their own category: *Proteus*, *E. coli*, *Pseudomonas*, *Klebsiella*, and *Legionella*.
5. Then the rest are Gram-negative rods with special considerations:
    a. Obligate intracellular organisms are *Chlamydia* and *Rickettsia*
    b. Spirochetes are Syphilis, Lyme, and Leptospirosis.
    c. Zoo bugs are *Yersinia pestis*, *Francisella*, *Brucella*, and *Pasteurella*
    d. Poop-disease bugs can cause dysentery (EHEC, *Shigella*, *Campylobacter*, *Y. enterocolitica*) or watery diarrhea (ETEC, *Vibrio cholerae*, *Salmonella not typhi*).
4. Oh, don't forget about *Mycobacterium*—TB, leprosy, and MAC.

Does it cover all the bacteria that there are? No. Does this explore the details of diseases these organisms cause? No. But we just took the infinite world of too many bugs to possibly study and boiled it down to "meh, not a bad list—I can manage this."